SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: BILLING-MEDEL, PATRICIA
                COHEN, MAURICE
                COLPITTS, TRACEY L.
                FRIEDMAN, PAULA N.
                GORDON, JULIAN
                GRANADOS, EDWARD N.
                HODGES, STEVEN C.
                KLASS, MICHAEL R.
                KRATOCHVIL, JON D.
                ROBERTS-RAPP, LISA
                RUSSELL, JOHN C.
                STROUPE, STEPHEN D.

(ii) TITLE OF THE INVENTION: REAGENTS AND METHODS USEFUL
        FOR DETECTING DISEASES OF THE PROSTATE

(iii) NUMBER OF SEQUENCES: 31

(iv) CORRESPONDENCE ADDRESS:
  (A) ADDRESSEE: Abbott Laboratories
  (B) STREET: 100 Abbott Park Road
  (C) CITY: Abbott Park
  (D) STATE: IL
  (E) COUNTRY: USA
  (F) ZIP: 60064-3500

(v) COMPUTER READABLE FORM:
  (A) MEDIUM TYPE: Diskette
  (B) COMPUTER: IBM Compatible
  (C) OPERATING SYSTEM: DOS
  (D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:
  (A) APPLICATION NUMBER:
  (B) FILING DATE:
  (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:
  (A) APPLICATION NUMBER: 08/856,653
  (B) FILING DATE: 15-MAY-1997

(viii) ATTORNEY/AGENT INFORMATION:
  (A) NAME: Becker, Cheryl L.
  (B) REGISTRATION NUMBER: 35,441
  (C) REFERENCE/DOCKET NUMBER: 6105.US.P1

(ix) TELECOMMUNICATION INFORMATION:
  (A) TELEPHONE: 847/935-1729
  (B) TELEFAX: 847/938-2623
  (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 290 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

  (ix) FEATURE:
    (A) NAME/KEY: base_polymorphism
    (B) LOCATION: 31
    (D) OTHER INFORMATION: /note= "'N' represents an A or G or
        T or C polymorphism at this position"

  (ix) FEATURE:
    (A) NAME/KEY: base_polymorphism
    (B) LOCATION: 232
    (D) OTHER INFORMATION: /note= "'N' represents an A or G or
        T or C polymorphism at this position"

  (ix) FEATURE:
    (A) NAME/KEY: base_polymorphism
    (B) LOCATION: 275
    (D) OTHER INFORMATION: /note= "'N' represents an A or G or
        T or C polymorphism at this position"

  (ix) FEATURE:
    (A) NAME/KEY: base_polymorphism
    (B) LOCATION: 284
    (D) OTHER INFORMATION: /note= "'N' represents an A or G or
        T or C polymorphism at this position"

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
CATTTGAGGC CATATAAAGT CACCTGAGGC NCTCTCCACC ACAGCCCACC AGTGACCATG      60
AAGGCTGTGC TGCTTGCCCT GTTGATGGCA GGCTTGGCCC TGCAGCCAGG CACTGCCCTG     120
CTGTGCTACT CCTGCAAAGC CCAGGTGAGC AACGAGGACT GCCTGCAGGT GGAGAACTGC     180
ACCCAGCTGG GGGAGCAGTG CTGGACCGCG CGCATCCGCG CAGTTGGCCT CNTGACCGTC     240
ATCAGCAAAG CTGCAGCTTG AACTGCGTGG ATGANTCACA GGANTACTAC                290
```

    (2) INFORMATION FOR SEQ ID NO:2:

  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 293 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
GAGGCCCTCT CCACCACAGC CCACCAGTGA CCATGAAGGC TGTGCTGCTT GCCCTGTTGA      60
TGGCAGGCTT GGCCCTGCAG CCAGGCACTG CCCTGCTGTG CTACTCCTGC AAAGCCCAGG     120
TGAGCAACGA GGACTGCCTG CAGGTGGAGA ACTGCACCCA GCTGGGGGAG CAGTGCTGGA     180
CCGCGCGCAT CCGCGCAGTT GGCCTCCTGA CCGTCATCAG CAAAGGCTGC AGCTTGAACT     240
GCGTGGATGA CTCACAGGAC TACTACGTGG GCAAGAAGAA CATCACGTGC TGT            293
```
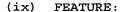
    (2) INFORMATION FOR SEQ ID NO:3:

  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 279 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```
CAGTGACCAT GAAGGCTGTG CTGCTTGCCC TGTTGATGGC AGGCTTGGCC CTGCAGCCAG    60
GCACTGCCCT GCTGTGCTAC TCCTGCAAAG CCCAGGTGAG CAACGAGGAC TGCCTGCAGG   120
TGGAGAACTG CACCCAGCTG GGGGAGCAGT GCTGGACCGC GCGCATCCGC GCAGTTGGCC   180
TCCTGACCGT CATCAGCAAA GGCTGCAGCT TGAACTGCGT GGATGACTCA CAGGACTACT   240
ACGTGGGCAA GAAGAACATC ACGTGCTGTG ACACCGACT                          279
```

        (2) INFORMATION FOR SEQ ID NO:4:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 207 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
GTGACCATGA AGGCTGTGCT GCTTGCCCTG TTGATGGCAG GCTTGGCCCT GCAGCCAGGC    60
ACTGCCCTGC TGTGCTACTC CTGCAAAGCC CAGGTGAGCA ACGAGGACTG CCTGCAGGTG   120
GAGAACTGCA CCCAGCTGGG GGAGCAGTGC TGGACCGCGC GCATCCGCGC AGTTGGCCTC   180
CTGACCGTCA TCAGCAAAGG CTGCAGC                                       207
```

        (2) INFORMATION FOR SEQ ID NO:5:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 265 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```
CGAGGACTGC CTGCAGGTGG AGAACTGCAC CCAGCTGGGG GAGCAGTGCT GGACCGCGCG    60
CATCCGCGCA GTTGGCCTCC TGACCGTCAT CAGCAAAGGC TGCAGCTTGA ACTGCGTGGA   120
TGACTCACAG GACTACTACG TGGGCAAGAA GAACATCACG TGCTGTGACA CCGACTTGTG   180
CAACGCCAGC GGGGCCCATG CCCTGCAGCC GGCTGCCGCC ATCCTTGCGC TGCTCCCTGC   240
ACTCGGCCTG CTGCTCTGGG GACCC                                         265
```

        (2) INFORMATION FOR SEQ ID NO:6:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 230 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```
GTGCTGTGAC ACCGACTTGT GCAACGCCAG CGGGGCCCAT GCCCTGCAGC CGGCTGCCGC    60
CATCCTTGCG CTGCTCCCTG CACTCGGCCT GCTGCTCTGG GGACCCGGCC AGCTATAGGC   120
TCTGGGGGGC CCCGCTGCAG CCCACACTGG GTGTGGTGCC CCAGGCCTCT GTGCCACTCC   180
TCACAGACCT GGCCCAGTGG GAGCCTGTCC TGGTTCCTGA GGCACATCCT              230
```

        (2) INFORMATION FOR SEQ ID NO:7:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 233 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

```
        (ix)  FEATURE:
              (A) NAME/KEY: base_polymorphism
              (B) LOCATION: 70
              (D) OTHER INFORMATION: /note= "'N' represents an A or G or
                  T or C polymorphism at this position"


        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CTGGCCCAGT GGGAGCCTGT CCTGGTTCCT GAGGCACATC CTAACGCAAG TCTGACCATG      60
TATGTCTGCN CCCCTGTCCC CCACCCTGAC CCTCCCATGG CCCTCTCCAG GACTCCCACC     120
CGGCAGATCA GCTCTAGTGA CACAGATCCG CCTGCAGATG GCCCCTCCAA CCCTCTCTGC     180
TGCTGTTTCC ATGGCCCAGC ATTCTCCACC CTTAACCCTG TGCTCAGGCA CCT           233


        (2)  INFORMATION FOR SEQ ID NO:8:

        (i)  SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 250 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: single
             (D) TOPOLOGY: linear

        (ix)  FEATURE:
              (A) NAME/KEY: base_polymorphism
              (B) LOCATION: 60
              (D) OTHER INFORMATION: /note= "'N' represents an A or G or
                   T or C polymorphism at this position"

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GTCCTGGTTC CTGAGGCACA TCCTAACGCA AGTCTGACCA TGTATGTCTG CACCCCTGTN      60
CCCCACCCTG ACCCTCCCAT GGCCCTCTCC AGGACTCCCA CCCGGCAGAT CAGCTCTAGT     120
GACACAGATC CGCCTGCAGA TGGCCCCTCC AACCCTCTCT GCTGCTGTTT CCATGGCCCA     180
GCATTCTCCA CCCTTAACCC TGTGCTCAGG CACCTCTTCC CCCAGGAAGC CTTCCCTGCC     240
CACCCCATCT                                                            250


        (2)  INFORMATION FOR SEQ ID NO:9:

        (i)  SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 259 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: single
             (D) TOPOLOGY: linear


        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TAACCCTGTG CTCAGGCACC TCTTCCCCCA GGAAGCCTTC CCTGCCCACC CCATCTATGA      60
CTTGAGCCAG GTCTGGTCCG TGGTGTCCCC CGCACCCAGC AGGGGACAGG CACTCAGGAG     120
GGCCCAGTAA AGGCTGAGAT GAAGTGGACT GAGTAGAACT GGAGGACAAG AGTCGACGTG     180
AGTTCCTGGG AGTCTCCAGA GATGGGGCCT GGAGGCCTGG AGGAAGGGGC CAGGCCTCAC     240
ATTCGTGGGG CTCCCTGAA                                                  259


        (2)  INFORMATION FOR SEQ ID NO:10:

        (i)  SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 253 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: single
             (D) TOPOLOGY: linear


        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATCTATGACT TGAGCCAGGT CTGGTCCGTG GTGTCCCCCG CACCCAGCAG GGGACAGGCA      60
CTCAGGAGGG CCCAGTAAAG GCTGAGATGA AGTGGACTGA GTAGAACTGG AGGACAAGAG     120
```
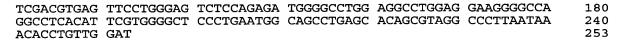
```
TCGACGTGAG TTCCTGGGAG TCTCCAGAGA TGGGGCCTGG AGGCCTGGAG GAAGGGGCCA    180
GGCCTCACAT TCGTGGGGCT CCCTGAATGG CAGCCTGAGC ACAGCGTAGG CCCTTAATAA    240
ACACCTGTTG GAT                                                        253
```

            (2) INFORMATION FOR SEQ ID NO:11:

            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 1023 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: single
                (D) TOPOLOGY: linear

            (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

```
CATTTGAGGC CATATAAAGT CACCTGAGGC CCTCTCCACC ACAGCCCACC AGTGACCATG     60
AAGGCTGTGC TGCTTGCCCT GTTGATGGCA GGCTTGGCCC TGCAGCCAGG CACTGCCCTG    120
CTGTGCTACT CCTGCAAAGC CCAGGTGAGC AACGAGGACT GCCTGCAGGT GGAGAACTGC    180
ACCCAGCTGG GGGAGCAGTG CTGGACCGCG CGCATCCGCG CAGTTGGCCT CCTGACCGTC    240
ATCAGCAAAG GCTGCAGCTT GAACTGCGTG GATGACTCAC AGGACTACTA CGTGGGCAAG    300
AAGAACATCA CGTGCTGTGA CACCGACTTG TGCAACGCCA GCGGGGCCCA TGCCCTGCAG    360
CCGGCTGCCG CCATCCTTGC GCTGCTCCCT GCACTCGGCC TGCTGCTCTG GGGACCCGGC    420
CAGCTATAGG CTCTGGGGGG CCCCGCTGCA GCCCACACTG GGTGTGGTGC CCCAGGCCTC    480
TGTGCCACTC CTCACAGACC TGGCCCAGTG GGAGCCTGTC CTGGTTCCTG AGGCACATCC    540
TAACGCAAGT CTGACCATGT ATGTCTGCAC CCCTGTCCCC CACCCTGACC CTCCCATGGC    600
CCTCTCCAGG ACTCCCACCC GGCAGATCAG CTCTAGTGAC ACAGATCCGC CTGCAGATGG    660
CCCCTCCAAC CCTCTCTGCT GCTGTTTCCA TGGCCCAGCA TTCTCCACCC TTAACCCTGT    720
GCTCAGGCAC CTCTTCCCCC AGGAAGCCTT CCCTGCCCAC CCCATCTATG ACTTGAGCCA    780
GGTCTGGTCC GTGGTGTCCC CCGCACCCAG CAGGGGACAG GCACTCAGGA GGGCCCAGTA    840
AAGGCTGAGA TGAAGTGGAC TGAGTAGAAC TGGAGGACAA GAGTCGACGT GAGTTCCTGG    900
GAGTCTCCAG AGATGGGGCC TGGAGGCCTG GAGGAAGGGG CCAGGCCTCA CATTCGTGGG    960
GCTCCCTGAA TGGCAGCCTG AGCACAGCGT AGGCCCTTAA TAAACACCTG TTGGATAAGC   1020
CCA                                                                 1023
```

            (2) INFORMATION FOR SEQ ID NO:12:

            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 1023 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: single
                (D) TOPOLOGY: linear

            (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

```
CATTTGAGGC CATATAAAGT CACCTGAGGC CCTCTCCACC ACAGCCCACC AGTGACCATG     60
AAGGCTGTGC TGCTTGCCCT GTTGATGGCA GGCTTGGCCC TGCAGCCAGG CACTGCCCTG    120
CTGTGCTACT CCTGCAAAGC CCAGGTGAGC AACGAGGACT GCCTGCAGGT GGAGAACTGC    180
ACCCAGCTGG GGGAGCAGTG CTGGACCGCG CGCATCCGCG CAGTTGGCCT CCTGACCGTC    240
ATCAGCAAAG GCTGCAGCTT GAACTGCGTG GATGACTCAC AGGACTACTA CGTGGGCAAG    300
AAGAACATCA CGTGCTGTGA CACCGACTTG TGCAACGCCA GCGGGGCCCA TGCCCTGCAG    360
CCGGCTGCCG CCATCCTTGC GCTGCTCCCT GCACTCGGCC TGCTGCTCTG GGGACCCGGC    420
CAGCTATAGG CTCTGGGGGG CCCCGCTGCA GCCCACACTG GGTGTGGTGC CCCAGGCCTC    480
TGTGCCACTC CTCACAGACC TGGCCCAGTG GGAGCCTGTC CTGGTTCCTG AGGCACATCC    540
TAACGCAAGT CTGACCATGT ATGTCTGCAC CCCTGTCCCC CACCCTGACC CTCCCATGGC    600
CCTCTCCAGG ACTCCCACCC GGCAGATCAG CTCTAGTGAC ACAGATCCGC CTGCAGATGG    660
CCCCTCCAAC CCTCTCTGCT GCTGTTTCCA TGGCCCAGCA TTCTCCACCC TTAACCCTGT    720
GCTCAGGCAC CTCTTCCCCC AGGAAGCCTT CCCTGCCCAC CCCATCTATG ACTTGAGCCA    780
GGTCTGGTCC GTGGTGTCCC CCGCACCCAG CAGGGGACAG GCACTCAGGA GGGCCCAGTA    840
AAGGCTGAGA TGAAGTGGAC TGAGTAGAAC TGGAGGACAA GAGTCGACGT GAGTTCCTGG    900
GAGTCTCCAG AGATGGGGCC TGGAGGCCTG GAGGAAGGGG CCAGGCCTCA CATTCGTGGG    960
GCTCCCTGAA TGGCAGCCTG AGCACAGCGT AGGCCCTTAA TAAACACCTG TTGGATAAGC   1020
CCA                                                                 1023
```

            (2) INFORMATION FOR SEQ ID NO:13:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 68 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AGCTCGGAAT TCCGAGCTTG GATCCTCTAG AGCGGCCGCC GACTAGTGAG CTCGTCGACC   60
CGGGAATT   68

            (2) INFORMATION FOR SEQ ID NO:14:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 68 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AATTAATTCC CGGGTCGACG AGCTCACTAG TCGGCGGCCG CTCTAGAGGA TCCAAGCTCG   60
GAATTCCG   68

            (2) INFORMATION FOR SEQ ID NO:15:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 24 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

AGCGGATAAC AATTTCACAC AGGA   24

            (2) INFORMATION FOR SEQ ID NO:16:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 18 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TGTAAAACGA CGGCCAGT   18

            (2) INFORMATION FOR SEQ ID NO:17:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 20 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GTGGGCAAGA AGAACATCAC   20

            (2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 22 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CGCAAGTCTG ACCATGTATG TC   22

    (2) INFORMATION FOR SEQ ID NO:19:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GCTGAGATGA AGTGGACTGA   20

    (2) INFORMATION FOR SEQ ID NO:20:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 21 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CAGACCTGGC TCAAGTCATA G   21

    (2) INFORMATION FOR SEQ ID NO:21:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

TAGGATGTGC CTCAGGAACC   20

    (2) INFORMATION FOR SEQ ID NO:22:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TTCTTGCCCA CGTAGTAGTC   20

    (2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 20 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TGACACCGAC TTGTGCAACG   20

        (2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 26 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TCGACTCTTG TCCTCCAGTT CTACTC   26

        (2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 123 amino acids
    (B) TYPE: amino acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Met Lys Ala Val Leu Leu Ala Leu Leu Met Ala Gly Leu Ala Leu Gln
 1   5   10   15
Pro Gly Thr Ala Leu Leu Cys Tyr Ser Cys Lys Ala Gln Val Ser Asn
            20   25   30
Glu Asp Cys Leu Gln Val Glu Asn Cys Thr Gln Leu Gly Glu Gln Cys
            35   40   45
Trp Thr Ala Arg Ile Arg Ala Val Gly Leu Leu Thr Val Ile Ser Lys
    50   55   60
Gly Cys Ser Leu Asn Cys Val Asp Asp Ser Gln Asp Tyr Tyr Val Gly
65   70   75   80
Lys Lys Asn Ile Thr Cys Cys Asp Thr Asp Leu Cys Asn Ala Ser Gly
                85   90   95
Ala His Ala Leu Gln Pro Ala Ala Ala Ile Leu Ala Leu Leu Pro Ala
            100   105   110
Leu Gly Leu Leu Leu Trp Gly Pro Gly Gln Leu
        115   120

        (2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 34 amino acids
    (B) TYPE: amino acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

```
Thr Ala Leu Leu Cys Tyr Ser Cys Lys Ala Gln Val Ser Asn Glu Asp
1               5                   10                  15
Cys Leu Gln Val Glu Asn Cys Thr Gln Leu Gly Glu Gln Cys Trp Thr
            20                  25                  30
Ala Arg
```

(2) INFORMATION FOR SEQ ID NO:27:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 41 amino acids
      (B) TYPE: amino acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: None

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

```
Arg Ile Arg Ala Val Gly Leu Leu Thr Val Ile Ser Lys Gly Cys Ser
1               5                   10                  15
Leu Asn Cys Val Asp Asp Ser Gln Asp Tyr Tyr Val Gly Lys Lys Asn
            20                  25                  30
Ile Thr Cys Cys Asp Thr Asp Leu Cys
        35                  40
```

(2) INFORMATION FOR SEQ ID NO:28:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 30 amino acids
      (B) TYPE: amino acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: None

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

```
Cys Val Asp Asp Ser Gln Asp Tyr Tyr Val Gly Lys Lys Asn Ile Thr
1               5                   10                  15
Cys Cys Asp Thr Asp Leu Cys Asn Ala Ser Gly Ala His Ala
            20                  25                  30
```

(2) INFORMATION FOR SEQ ID NO:29:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 24 amino acids
      (B) TYPE: amino acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: None

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

```
Leu Gln Pro Ala Ala Ala Ile Leu Ala Leu Leu Pro Ala Leu Gly Leu
1               5                   10                  15
Leu Leu Trp Gly Pro Gly Gln Leu
            20
```

(2) INFORMATION FOR SEQ ID NO:30:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 8 amino acids
      (B) TYPE: amino acid
      (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Asp Tyr Lys Asp Asp Asp Asp Lys
1   5

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Met His Thr Glu His
1   5   10   15
His His His His His
        20